

+

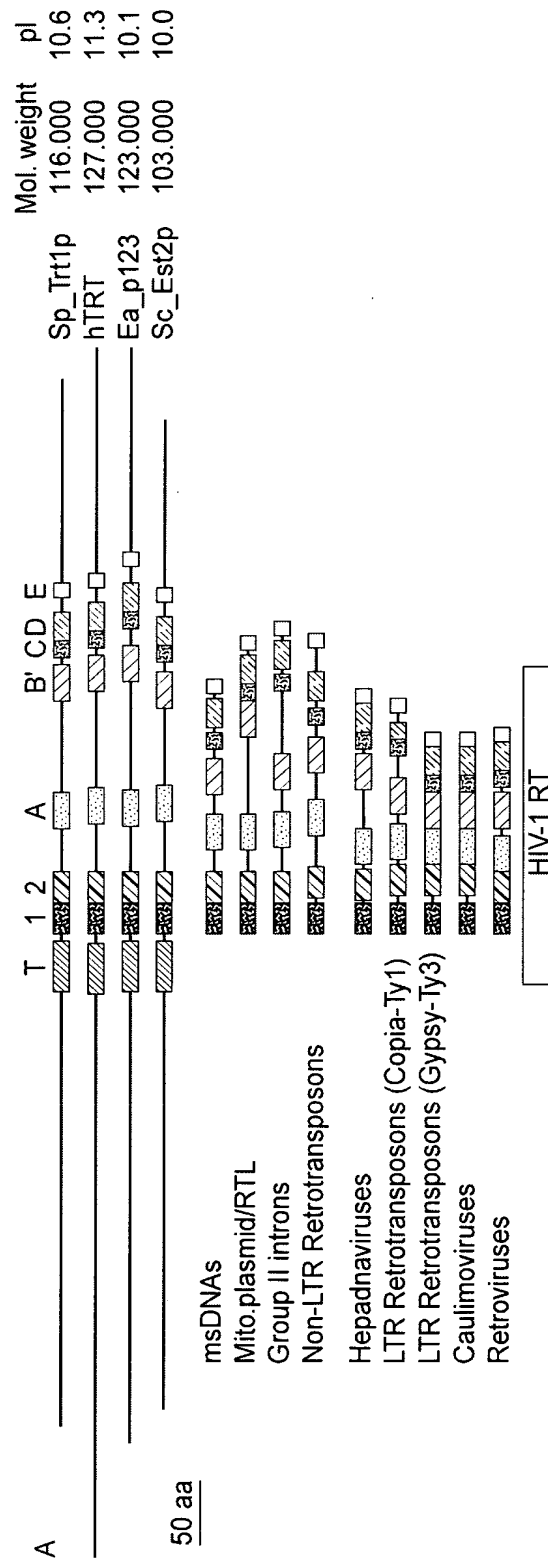


FIG. 2

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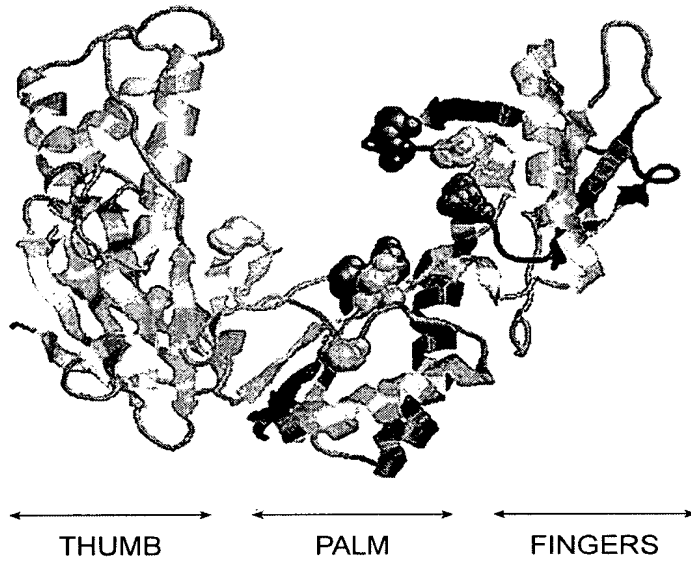


FIG. 3

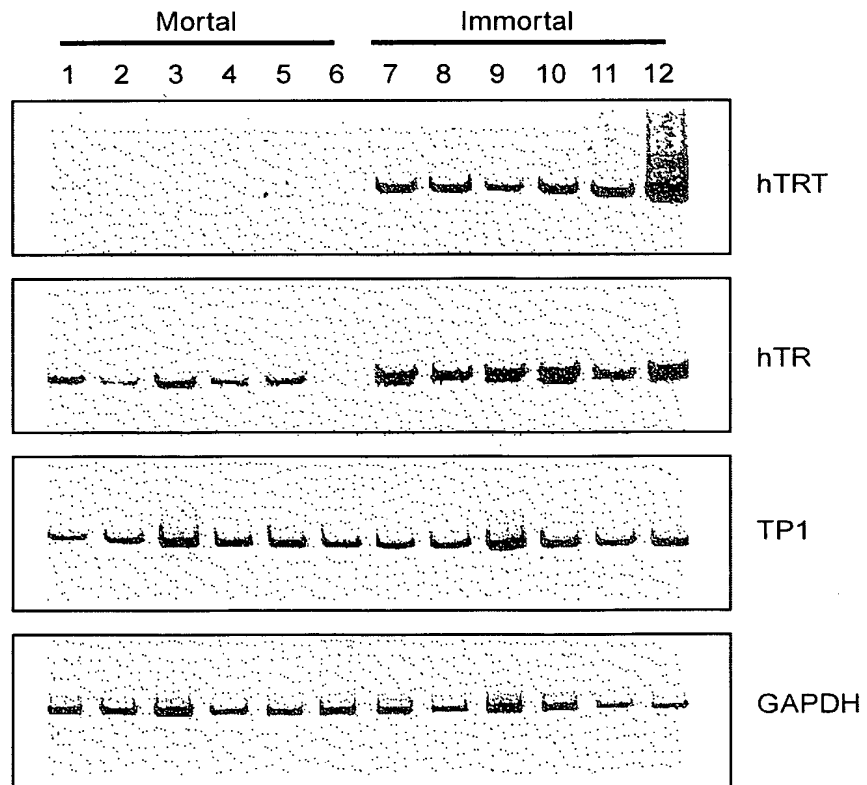


FIG. 5

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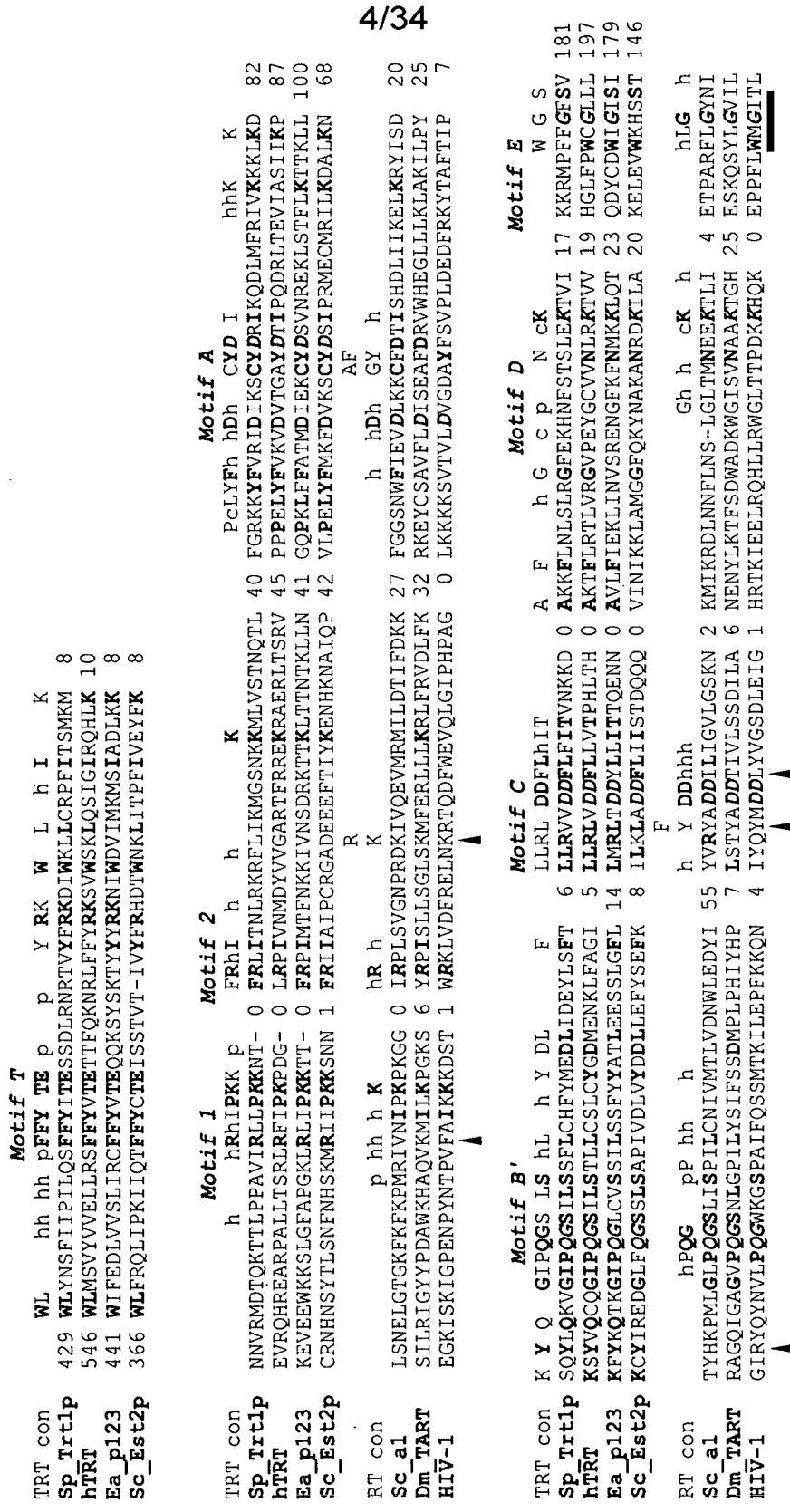


FIG. 4

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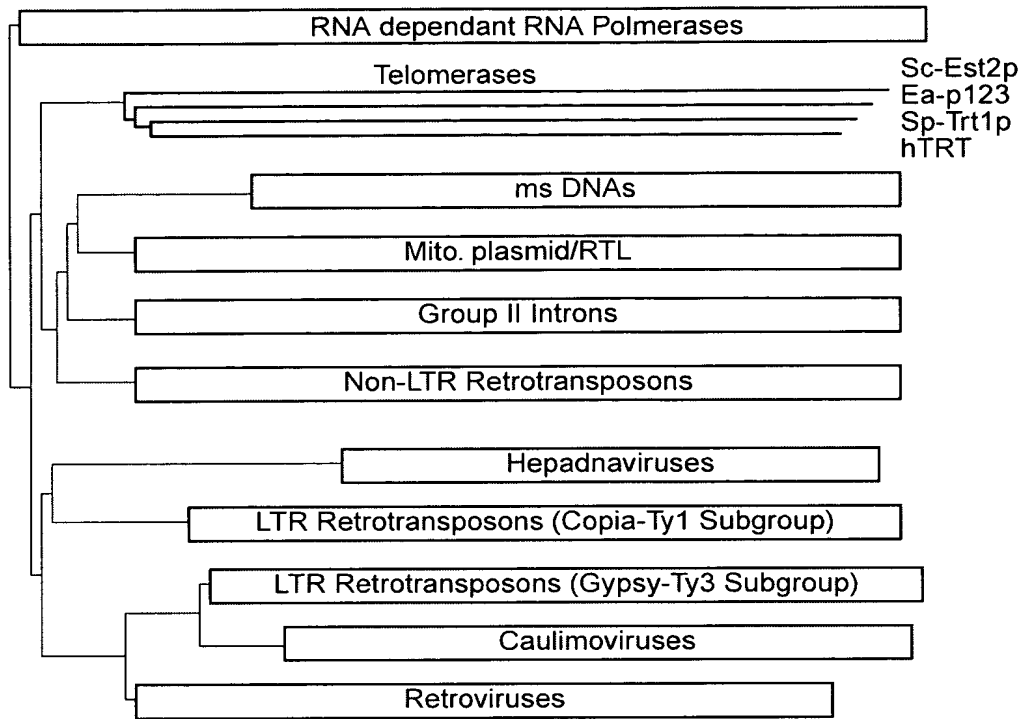


FIG. 6

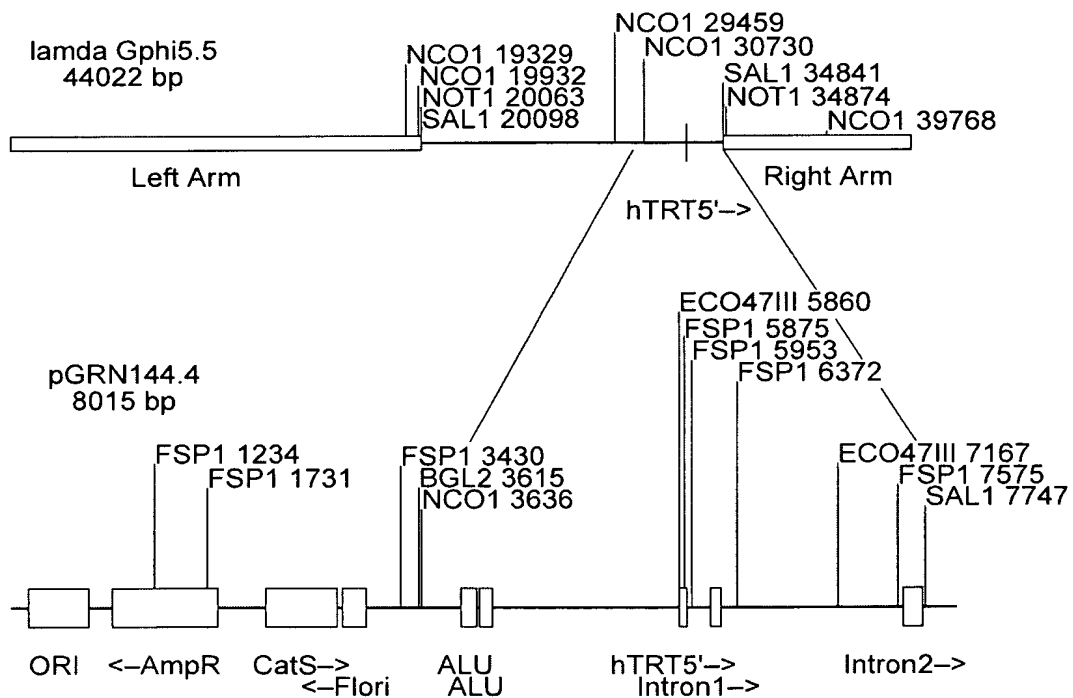


FIG. 7

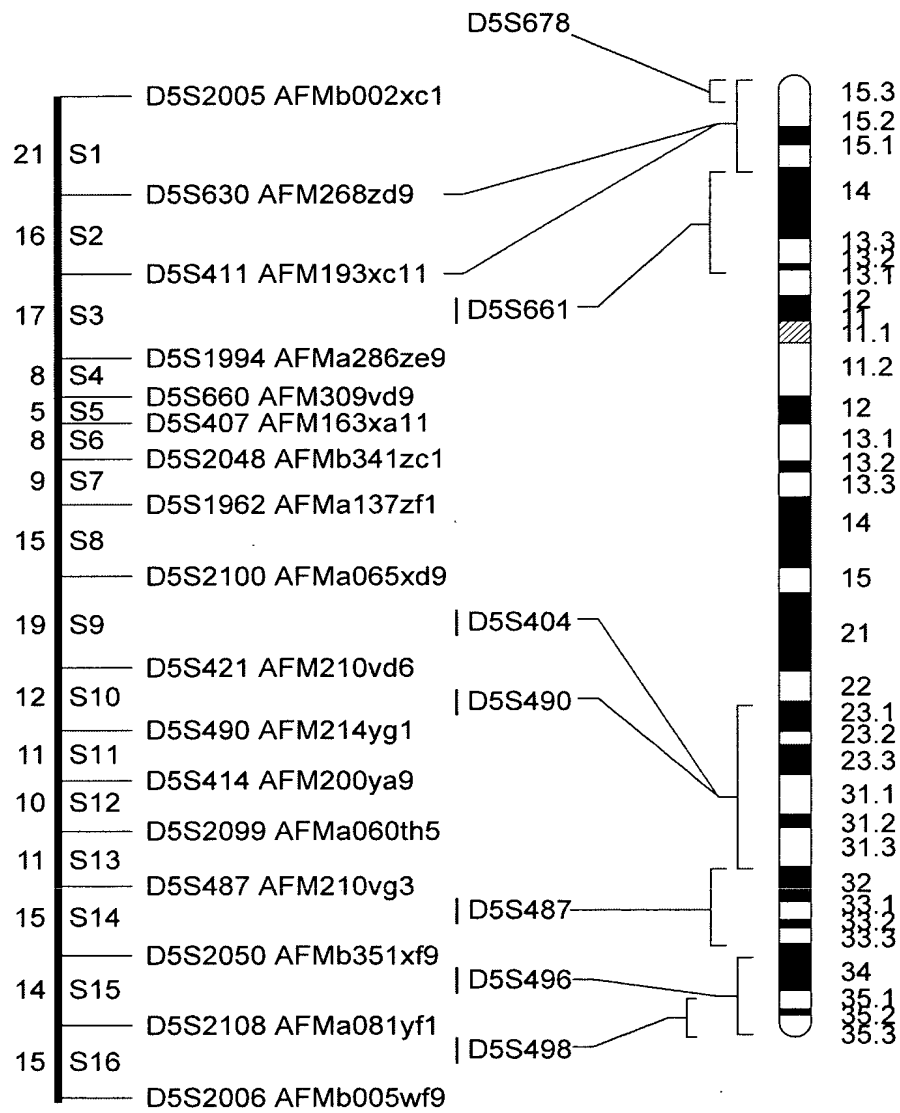


FIG. 8

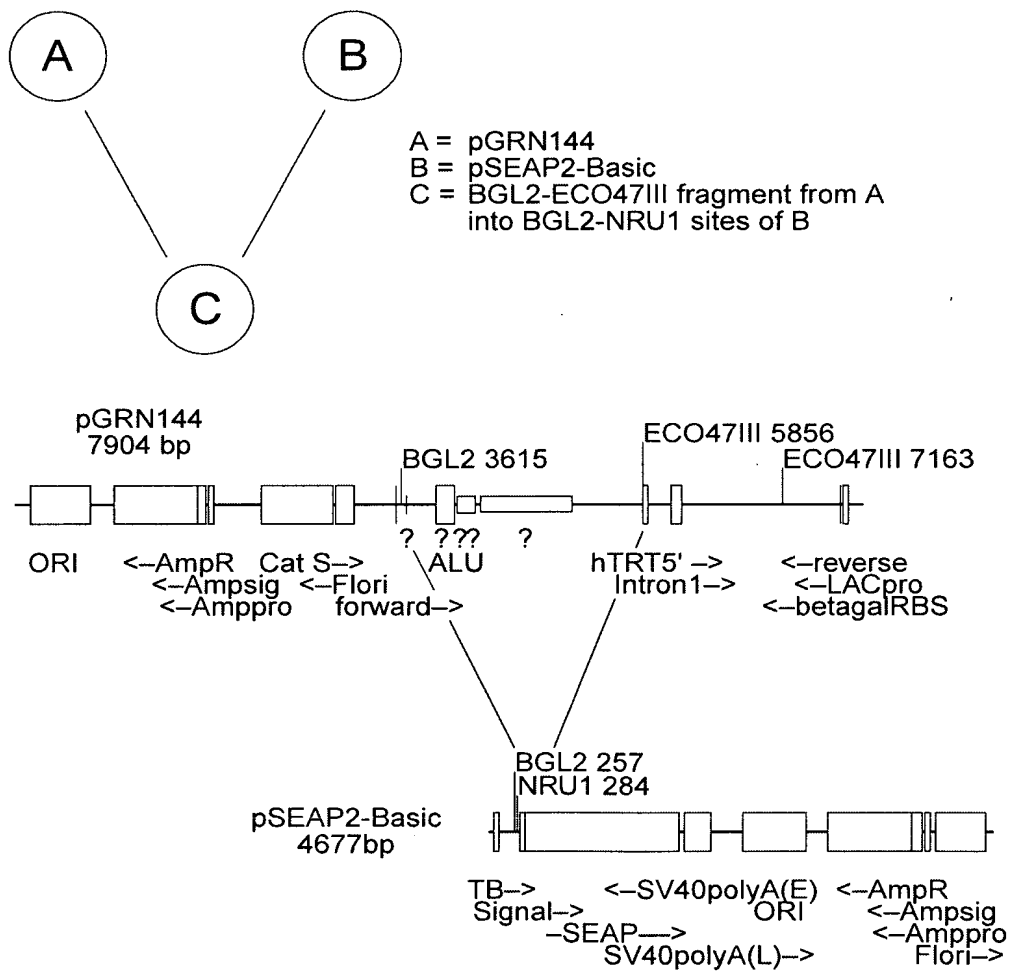


FIG. 9

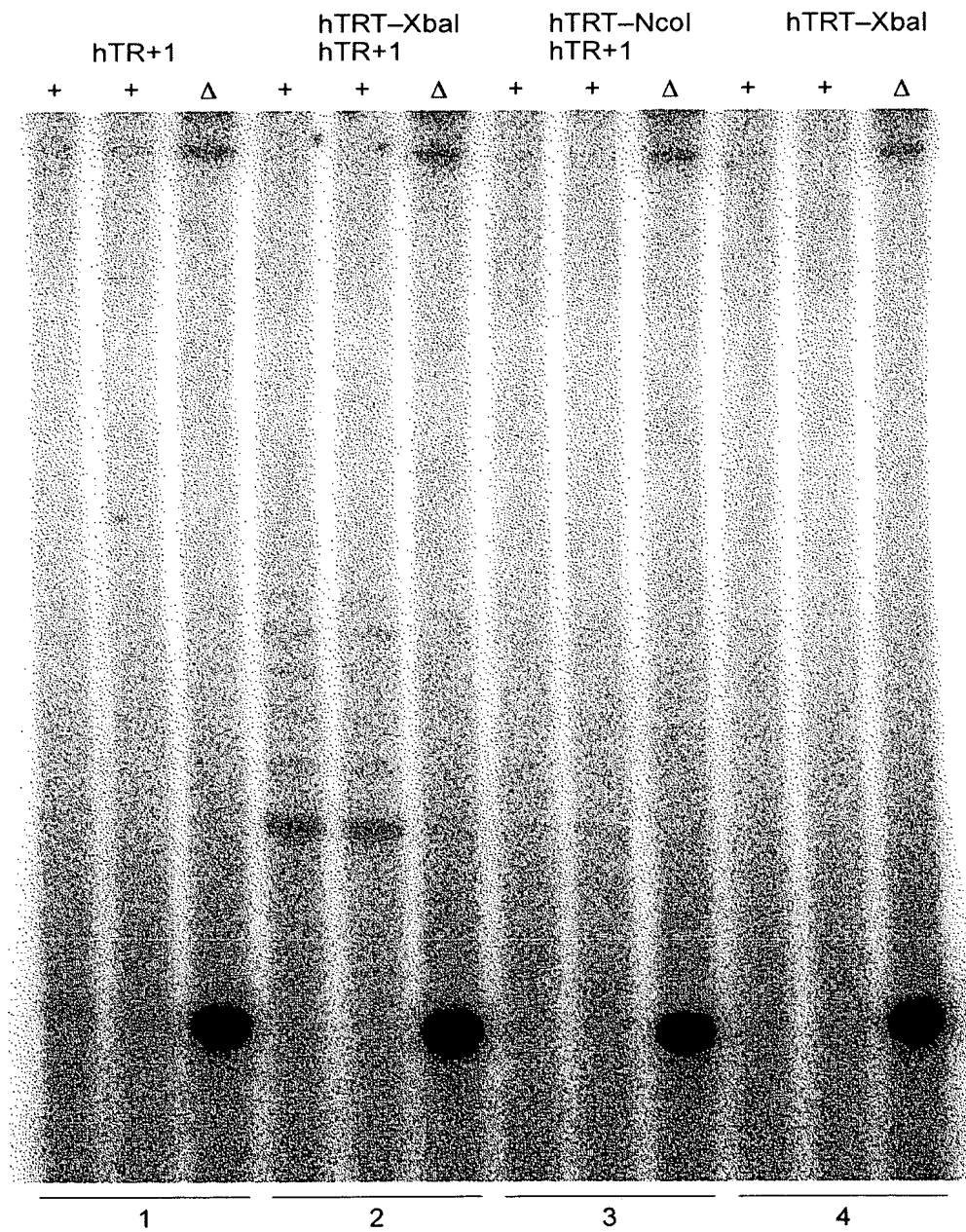


FIG. 10A

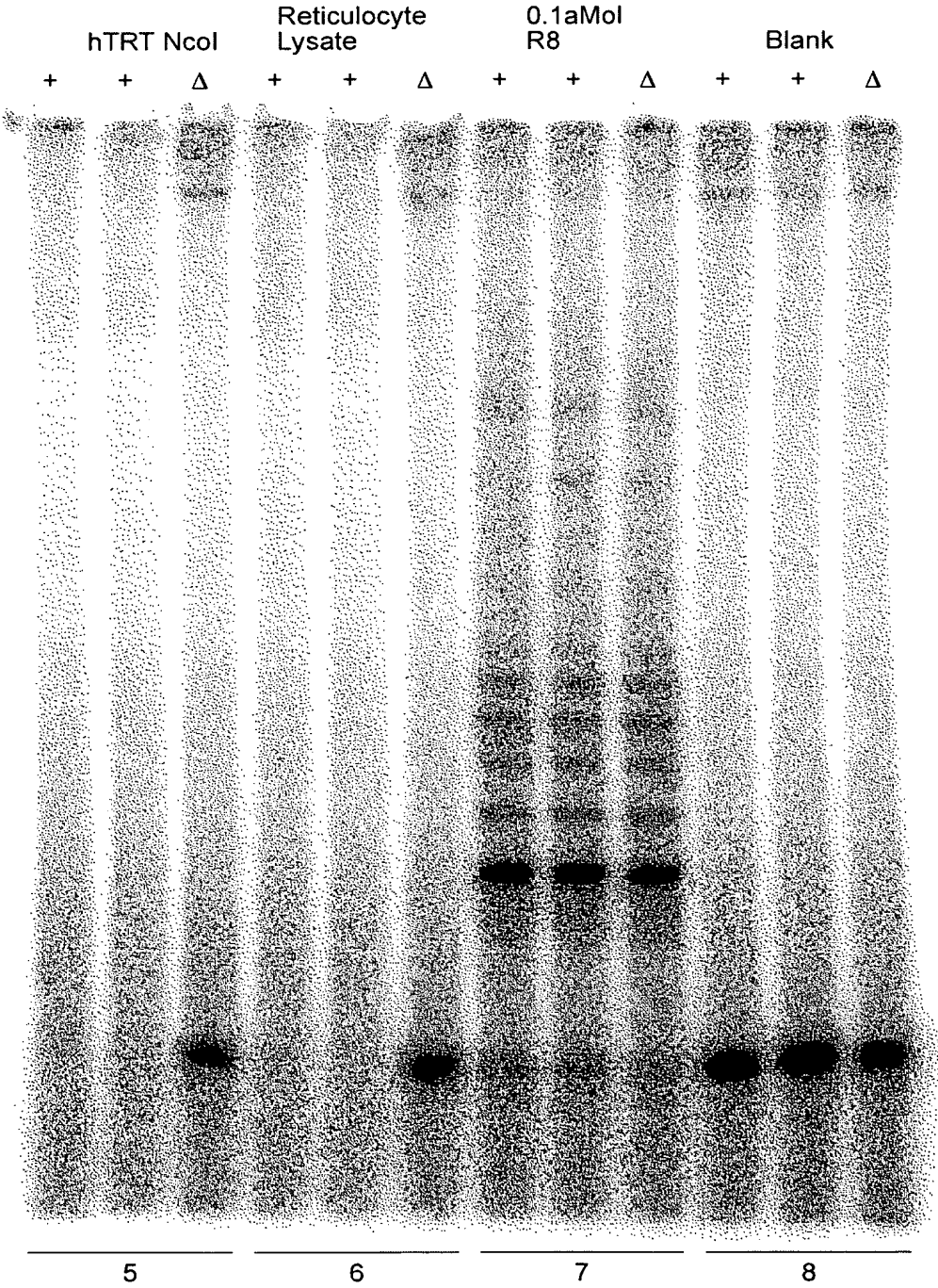


FIG. 10B

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Telomerase Specific Motifs

	MOTIF T	MOTIF T'
TRT con	W1	
hTRT	546 WLMVVVVELLRFFVVTETTTQKNRFFYRKSVWSKLQSIGI	13 EAEVR
spTRT	429 WLYNSFIIPILQSFYITESSDLNRRTVYFRKDIWKLRCRPI	12 ENNVR
Ea_p123	441 WIFEDLVVSLIRCFYVTEQQKSYKTYYYRKNIDVIMKMSI	12 EKEVE
Sc_Est2	366 WLFRLIPKIIQTFYCTEISSTVT.IVYFRHDTWNKLITPFI	9 ENNVC

Telomerase RT Motifs (Fingers)

	MOTIF 1	MOTIF 2	MOTIF A	MOTIF B'
TRT con	R iPKk	fr I	p lyF D cyd i	Y q GIPQGs ls l Y
hTRT	11 SRLRFIPKPDG 0 LRPIV	69 PELYFVKVDVTGAYDTI	104 YVQCQGIPOGSILSTLLCSLCY	
spTRT	10 AVIRLLPKQNT 0 FRLIT	66 RKKYFVRIDIKSCYDRI	99 YLQKVGIPQGSILSSFLCHFYM	
Ea_p123	10 GKRLIPKKT 0 FRPIM	67 PKLFFATMDIEKCYDSV	117 YKQTKGIPQGLCVSSILSSFY	
Sc_Est2	13 SKMRIIPKSN 2 FRIIA	68 PELYFMKFDVKCYDSI	85 YIREDGLFQGSLSAPIVDLVY	
RT con	p hh h K	hR h	h hDh AF h	hPQG pP hh h
			GY	

Telomerase RT Motifs (Palm, Primer Grip)

	MOTIF C	MOTIF D	MOTIF E
TRT con	111rl Ddfl it	g	n k w g s l
hTRT	15 LLLRLVDDFLLV	15 GVPEYGCVVNLKRTVV	24 WCGLLLDTRTL 192
spTRT	16 VLLRVVDDFLFIT	15 GFEEKNFSTSLKTVI	22 FFGFSVNMRS 176
Ea_p123	24 LLMRLTDDYLLIT	15 VSRENGFKFNKKLQT	28 WIGISIDMKTL 174
Sc_Est2	18 LILKLADDFLIIS	15 GFQKYNKANRDKILA	25 WKHSSTMNPF 141
RT con	h Y DDhhh	Gh h ck h	hLG h
	F		

FIG. 11

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181 GGACCCGGCGGCTTTCCGCGCGCTGGTGGCCAGTGCCTGGTGTGCGTGCCCTGGGACGC
    CCTGGGCGCGCGAAAGGCGCGCGACACCGGGTCACGGACCACACGCACGGGACCCTGCG

                                NFkB_CS1
                                GGGRQTYYQC
                                NFkB-MHC-I.2
                                TGGGCTTCCCC
                                *****
241 ACGGCCGCCCCCGCCGCCCCCTCCTTCCGCCAGGTGGGCCTCCCCGGGGTCGGCGTCCG
    TGCCGGCGGGGGGCGGCGGGGGAGGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGC

                                Intron1
                                *****
301 GCTGGGGTTGAGGGCGGCCGGGGGGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTC
    CGACCCCAACTCCCGCCGGCCCCCCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAG

                                NFkB_CS1
                                GGGRQTYYQC
                                NFkB_CS2
                                RGGGRMTYYCC
                                Topo_II_cleavage_site
                                RNYNNC̄NNGYNGKT̄N̄NY
                                *****>
361 AGGGCGCTTCCCCCGCAGGTGTCCTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGG
    TCCCGCGAAGGGGGCGTCCACAGGACGGACTTCCTCGACCACCGGGCTCACGACGTCTCC
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FIG. 12

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1   AAAACCCCAA AACCCCAAAA CCCCTTTTAG AGCCCTGCAG TTGGAAATAT
51  AACCTCAGTA TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA
101 ATGGAGGTTG ATGTTGATAA TCAAGCTGAT AATCATGGCA TTCCTCAGC
151 TCTTAAGACT TGTGAAGAAA TTAAAGAAGC TAAAACGTTG TACTCTTGG
201 TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA TTATAAAGAT
251 TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG
301 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT
351 CAACTGGACT AATGATCGAA CTTATTGACA AATGCTTAGT TGAAGTTCTT
401 TCATCAAGCG ATGTTTCAGA TAGACAAAAA CTTCAATGAT TTGGATTTC
451 ACTTAAGGGA AATCAATTAG CAAAGACCCA TTTATTAACA GCTCTTTCAA
501 CTCAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT TAGAGCAATG
551 ATTGGAAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA
601 GCGAAGTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG
651 ATCATTTGAA AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA
701 GCAGACATGA ATGAACCTCG ATGTTGATCA ACCTGCAAAAT ACAATGTCAA
751 GAATGAGAAA GATCACTTTC TCAACAACAT CAACGTGCCG AATTGGAATA
801 ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATT TAATAGAAAT
851 AACCAATTCT TCAAAAAGCA TGAGTTTGTA AGTAACAAAA ACAATATTTT
901 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA
951 GAATTAGAAA GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG
1001 CTTGAGAAAG TCAAAGATTT TAACCTCAAC TACTATTTAA CAAAATCTTG
1051 TCCTCTTCCA GAAATTGGC GGAACGGAA ACAAAAAATC GAAACTTGA
1101 TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA GCTGTTAGC
1151 TACACAACTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTCTA
1201 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC
1251 AAAAGAAAGT TAAGAAATAT GTGGAAGTAA ACAAGCATGA ACTCATTAC
1301 AAAAAGTTAT TGCTTGAGAA GATCAATACA AGAGAAATAT CATGGATGCA
1351 GGTGAGACC TCTGCAAAGC ATTTTTATTA TTTTGATCAC GAAAACATCT
1401 ACGTCTTATG GAAATTGCTC CATTGGATAT TCGAGGATCT CGTCGTCTCG
1451 CTGATTAGAT GATTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA
1501 AACCTATTAC TACAGAAAGA ATATTTGGGA CGTCATTATG AAAATGTCAA
1551 TCGCAGACTT AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT
1601 GAAGAATGGA AAAAGTCGCT TGGATTTGCA CCTGGAAAAC TCAGACTAAT
1651 ACCGAAGAAA ACTACTTTCC GTCCAATTAT GACTTTCAAT AAGAAGATTG
1701 TAAATTCAGA CCGGAAGACT ACAAATTAAC CTACAAATAC GAAGTTATTG
1751 AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC
1801 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG
1851 AGTTTGTTTG CAAATGGAAG CAAGTTGGAC AACCAGAACT CTTCTTTGCA
1901 ACTATGGATA TCGAAAAGTG ATATGATAGT GTAAACAGAG AAAAAGTATC
1951 AACATTCCTA AAAACTACTA AATTACTTTC TTCAGATTTC TGGATTATGA
2001 CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA TTCGAAAAAC
2051 TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT
2101 TGCACTTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG
2151 AACAAAATGA CTTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA
2201 AGAAATTATT TTAAGAAAGA TAACCTACTT CAACCAGTCA TTAATATTTG
2251 CCAATATAAT TACATTAAC TTAATGGGAA GTTTTATAAA CAAACAAAAG
2301 GAATTCCTCA AGGTCTTTGA TTTTCATCAA TTTTGTATC TTTTATTAT
2351 GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA

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FIG. 13A

2401	CCCTGAAAAT	CCAAATGTTA	ATCTTCTAAT	GAGACTTACA	GATGACTATC
2451	TTTTGATTAC	AACTCAAGAG	AATAATGCAG	TATTGTTTAT	TGAGAAACTT
2501	ATAAACGTAA	GTCGTGAAAA	TGGATTTAAA	TTCAATATGA	AGAAACTACA
2551	GACTAGTTTT	CCATTAAGTC	CAAGCAAATT	TGCAAAATAC	GGAATGGATA
2601	GTGTTGAGGA	GCAAAATATT	GTTCAAGATT	ACTGCGATTG	GATTGGCATC
2651	TCAATTGATA	TGAAAACCTCT	TGCTTTAATG	CCAAATATTA	ACTTGAGAAT
2701	AGAAGGAATT	CTGTGTACAC	TCAATCTAAA	CATGCAAACA	AAGAAAGCAT
2751	CAATGTGGCT	CAAGAAGAAA	CTAAAGTCGT	TTTTAATGAA	TAACATTACC
2801	CATTATTTTA	GAAAGACGAT	TACAACCGAA	GACTTTGCGA	ATAAACTCT
2851	CAACAAGTTA	TTTATATCAG	GCGGTTACAA	ATACATGCAA	TGAGCCAAAG
2901	AATACAAGGA	CCACTTTAAG	AAGAACTTAG	CTATGAGCAG	TATGATCGAC
2951	TTAGAGGTAT	CTAAAATTAT	ATACTCTGTA	ACCAGAGCAT	TCTTTAAATA
3001	CCTTGTGTGC	AATATTAAGG	ATACAATTTT	TGGAGAGGAG	CATTATCCAG
3051	ACTTTTTTCT	TAGCACACTG	AAGCACTTTA	TTGAAATATT	CAGCACAAAA
3101	AAGTACATTT	TCAACAGAGT	TTGCATGATC	CTCAAGGCAA	AAGAAGCAAA
3151	GCTAAAAAGT	GACCAATGTC	AATCTCTAAT	TCAATATGAT	GCATAGTCGA
3201	CTATTCTAAC	TTATTTTGGG	AAGTTAATTT	TCAATTTTTG	TCTTATATAC
3251	TGGGGTTTTG	GGGTTTTTGG	GTTTTTGGG		

FIG. 13B

1	MEVDVDNQAD	NHGIHSALKT	CEEIKEAKTL	YSWIQKVIRC	RNQSQSHYKD
51	LEDIKIFAQT	NIVATPRDYN	EEDFKVIARK	EVFSTGLMIE	LIDKCLVELL
101	SSSDVSDRQK	LQCFGFQLKG	NQLAKTHLLT	ALSTQKQYFF	QDEWNQVRAM
151	IGNELFRHLY	TKYLIFQRTS	EGTLVQFCGN	NVFDHLKVND	KFDKKQKGGA
201	ADMNEPRCCS	TCKYNVKNK	DHFLNNINVP	NWNNMKSRT	IFYCTHFNRN
251	NQFFKKHEFV	SNKNNISAMD	RAQTIFTNIF	RFNRIRKKLK	DKVIEKIAM
301	LEKVKDFNFN	YYLTKSCPLP	ENWRERKQKI	ENLINKTREE	KSKYEEELFS
351	YTTDNKCVTQ	FINEFFYNIL	PKDFLTGRNR	KNFQKKVKKY	VELNKHELH
401	KNLLLEKINT	REISWMQVET	SAKHFFYFDH	ENIYVLWKLL	RWIFEDLVVS
451	LIRCFYVTE	QQKSYSKTY	YRKNIWDVIM	KMSIADLKKE	TLAEVQEKEV
501	EEWKSLGFA	PGKLRLIPKK	TTFRPIMTFN	KKIVNSDRKT	TKLTTNTKLL
551	NSHLMLKTLK	NRMFKDPFGF	AVFNYDDVMK	KYEEFVCKWK	QVGQPKLFFA
601	TMDIEKCYDS	VNREKLSTFL	KTTKLLSSDF	WIMTAQILKR	KNNIVIDSKN
651	FRKKEMKDIF	RQKFQKIALE	GGQYPTLFSV	LENEQNDLNA	KKTLIVEAKQ
701	RNYFKKDNLL	QPVINICQYN	YINFNGKFYK	QTKGIPQGLC	VSSILSSFYY
751	ATLEESSLGF	LRDESMNPEN	PNVNLLMRLT	DDYLLITTQE	NNAVLFIEKL
801	INVSRENGFK	FNMKKLQTSF	PLSPSKFAKY	GMDSVEEQNI	VQDYCDWIGI
851	SIDMKTLALM	PNINLRIEGI	LCTLNLNMQT	KKASMWLKKK	LKSFLMNNIT
901	HYFRKTTITE	DFANKTLNKL	FISGGYKYM	CAKEYKDHFK	KNLAMSSMID
951	LEVSKIIYSV	TRAFFKYLVC	NIKDTIFGEE	HYPDFFLSTL	KHFIEIFSTK
1001	KYIFNRVCM	LKAKEAKLKS	DQCQSLIQYD	A	

FIG. 14

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1  ggtaccgatttacttcttcttccataagcctaattgcttctcctcgaaacgctcctaataatcttgaaatatttttacaaga 80
81  actcaataacaataccaaagtaattccaaattcgaatgaaggtgtattatgtagtgatgaataatttctatttcggtcggtta 160
161  ccaagtataagcaaaaaaagaacaacttctctcccccctaaagacattttactatttataatttctatttcaaatatttcg 240
241  ggttcgcttacttttaactcgttgtagtcttctagcgaacccggtgttctaccccgatggataat 320
321  agtcttgtagtagctcacagaataccttacaatacttctgtaggagactatattagattcattacagtcggtgcataatc 400
401  ttaacatggagccttacacttttagatgagtcacgtcgcatgagtgagtagtttgtagtccatcaacggttgccttgaaaag 480
481  gttgataattattgcaaaaatcattccttagtggtggttaacccggaagtttttggatcgcacacggttcagcatg 560
561  attgagataattcaaaaatcttctaccatacaactcctttaacgcggttttatttttctatttctattcctcatgtgtt 640
641  ccaaatatgtatcgtattaggtttttccggttttactcctggaatcctggaacggttttctactattcccttaataga 720
721  ataactcaaatagtttcgcttataaattgtagtagtagagaagattggtgattcctactcgtgtaattgtagtttaaa 800
801  gatactttgcaaaaacatttattagctatcattatataaaaaaacctataattataaaatcaatatttgcggtc 880
881  actatttttaaaaacggttatgatcagtaggacactttgcatatatatgattatgcttaattggttacttgtaacttgc 958

959  ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA 1018
1 M T E H H T P K S R I L R F L E N Q Y V 20

1019  TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG 1078
21 Y L C T L N D Y V Q L V L R G S P A S S 40

1079  TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT 1138
41 Y S N I C E R L R S D V Q T S F S I F L 60

1139  CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA 1198
61 H S T V V G F D S K P D E G V Q F S S P 80

1199  AAA TGC TCA CAG TCA GAG gtatatatatttttgttttggatttttttctatttcgggatagctaataatgggcag 1272
81 K C S Q S E 86

1273  CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA 1332
87 L I A N V V K Q M F D E S F E R R N L 106

1333  CTG ATG AAA GGG TTT TCC ATG gtaagggtattcctaattgtgaaatatttacctgcaattactgtttcaagaga 1405
107 L M K G F S M 113

1406  ttgtatttaaccgataaaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GCA GTA CAA AAT 1469
N H E D F R A M H V N G V Q N 128
114

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FIG. 15A

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1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
 129 D L V S T F P N Y L I S I L E S K N W Q 148
 1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L L L E I I G 155
 1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
 156 S D A M H Y L L S K G S I F E A L P N D 175
 1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
 176 N Y L Q I S G I P L F K N N V F E T V 195
 1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
 196 S K K R K R T I E T S I T Q N K S A R K 215
 1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
 216 E V S W N S I S I S R F S I F Y R S S Y 235
 1842 AAG AAG TTT AAG CAA G gtaactaataactgttattccttcataactaatttttag AT CTA TAT TTT AAC 1907
 236 K K F K Q D L Y F N 245
 1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
 246 L H S I C D R N T V H M W L Q W I F P R 265
 1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
 266 Q F G L I N A F Q V K Q L H K V I P L V 285
 2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
 286 S Q S T V V P K R L L K V Y P L I E Q T 305
 2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
 306 A K R L H R I S L S K V Y N H Y C P Y I 325
 2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
 326 D T H D D E K I L S Y S L K P N Q V F A 345
 2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
 346 F L R S I L V R V F P K L I W G N Q R I 365

FIG. 15B

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2268 TTT GAG ATA ATA TTA AAA G gatttgataaaattttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F E I I L K D L E T 375
 2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG ACT AAC ATA AAG 2396
 376 F L K L S R Y E S F S L H Y L M S N I K 395
 2397 gtaatatgccaaattttttaccatttaataacaatcag ATT TCA GAA AIT GAA TGG CTA GTC CTT GGA 2465
 396 I S E I E W L V L G 405
 2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG 2525
 406 K R S N A K M C L S D F E K R K Q I F A 425
 2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT 2585
 426 E F I Y W L Y N S F I I P I L Q S F F Y 445
 2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA 2645
 446 I T E S S D L R N R T V Y F R K D I W K 465
 2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG 2705
 466 L L C R P F I T S M K M E A F E K I N E 485
 2706 gtattttaagtgatttttttgcaaaaagctaataatttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486 N N V R M D T Q K T 495
 2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG 2835
 496 T L P P A V I R L L P K K N T F R L I T 515
 2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtatttaatttttggtcatcaatgtactttacttctaatttatta 2906
 516 N L R K R F L I K 524
 2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG 2967
 525 M G S N K K M L V S T N Q T L R P V 542
 2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA AAG AGT AGT GGT ATT CCA TTT AAC TTG GAG 3027
 543 A S I L K H L I N E S S G I P F N L E 562
 3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V Y M K L L T F K K D L L K H R M F G 581

FIG. 15C

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3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA 3155
582      R K K Y F V R I D I 591
3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC 3215
592 K S C Y D R I K Q D L M F R I V K K L 611
3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT 3275
612 K D P E F V I R K Y A T I H A T S D R A 631
3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttccattggaattttttaaca 3343
632 T K N F V S E A F S Y F 643
3344 attcttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA 3405
644      D M V P F E K V V Q L L S M K T 659
3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT 3465
660 S D T L F V D F V D Y W T K S S E I F 679
3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgtgaattgtaataca 3532
680 K M L K E H L S G H I V K 692
3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA 3593
693      I G N S Q Y L Q K V G I P Q G S 708
3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG 3653
709 I L S S F L C H F Y M E D L I D E Y L S 728
3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA 3713
729 F T K K G S V L L R V V D D F L F I T 748
3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgcattcc 3777
749 V N K K D A K K F L N L S L R G 764
3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA 3840
765      F E K H N F S T S L E K T V 778
3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAA 3900
779 I N F E N S N G I I N N T F F N E S K K 798

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FIG. 15D

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3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT 3960
 799 R M P F F G F S V N M R S L D T L L A C 818

 3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG 4020
 819 P K I D E A L F N S T S V E L T K H M G 838

 4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
 839 K S F F Y K I L R S 848

 4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT 4149
 849 S L A S F A Q V F I D I T H N S K F N S 868

 4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA 4209
 869 C C N I Y R L G Y S M C M R A Q A Y L K 888

 4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtaacttattttaactaga 4274
 889 R M K D I F I P Q R M F I T D 903

 4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
 904 L L N V I G R K I W K K L A 917

 4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
 918 E I L G Y T S R R F L S S A E V K W 935

 4402 ggtctcgagacttcagcaaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA 4468
 936 L F C L G M R D G L K 946

 4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT 4528
 947 P S F K Y H P C F E Q L I Y Q F Q S L T 966

 4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA ATA 4588
 967 D L I K P L R P V L R Q V L F L H R R I 986

 4589 GCT GAT TAA tgtcatttttcaattattattatatacatcccttttattactggtgtcttaacaacaattattactaagtata 4665
 987 A D * 989

FIG. 15E

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4666 gctgacccccaaagcaagcatactataggatttcttagtaagtaaaataatctcgttatttagtttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtgggtgctgactactgccacatgccattaaacgggagtggttaaac 4825
4826 ttaaaagtaatacatgaggctaactccttctattagaataaggaaagtgggtttctataatgaataatgccgcacta 4905
4906 atgcaaaagacgaagatatcttctaaacaaggggatlaagcatatccgaaggaaagagagtaatataccagtgtt 4985
4986 gttgaagaaagcaaggataaatttggaacaagcttctgcagatgacaggctaaatttttggtgaccgaattttggtaaaagc 5065
5066 ccaggttatccatggtggccgacctgctactgagacgaaagaaactaaggatagtttgaatactaatagctcattta 5145
5146 atgtcttatataaggttttggtttctctgacttcaatttgcatgggtgaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaagcgggaagtctaaagaacttattgaagcttatgaggttcaaaaactcc 5305
5306 tcctgatttaaaggaggaaatcttccaccgatgaggaaatggatagcttaccgtctgaggagaagcctaattttttgc 5385
5386 aaaaagaaaatatcatgggagacatctcttgatgaatcagatcgggagagtatctccagcggatcccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgttctgacttctcgtagctctacgcagttaagtacccaaagggtacc 5544

FIG. 15F

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1 gcagcgctgc gtccctgctgc gcaagtgagg agccctggcc cgggccaccc ccgcgatgcc
61 gcgcgctccc cgctgcccag ccgtgcccgc cctgctgccc agccactacc gcgaggtgct
121 gccgctggcc acgttcctgc ggcgcctggg gccccagggg tggcggctgg tgccagcgcg
181 ggacccggcg gctttccgcg cgctgggtgg ccagtgcctg gtgtgctgct cctgggacgc
241 acggccgccc cccgcccggc cctccttccg ccaggtgtcc tgctgaagg agctgggtgg
301 ccgagtgctg cagaggctgt ggcagcgccc cgcgaagaac gtgctggcct tcggcttcgc
361 gctgctggac ggggcccgcg ggggccttcc cgaggccttc accaccagcg tgcgcagcta
421 cctgcccac acggtgacgg acgcaactgc ggggagcggg gcgtgggggc tgctgctgct
481 ccgctggggc gacgacgtgc tggttcacct gctggcacgc tgcgcgctct ttgtgctggt
541 ggctcccagc tgcgcctacc aggtgtgccc gccgcgctg taccagctcg gcgctgccac
601 tcaggcccgg cccccgccac acgctagtgg accccgaagg cgtctgggat gcgaacgggc
661 ctggaaccat agcgtcaggg aggcgggggt ccccttgggc ctgccagccc cgggtgagag
721 gaggcgcccc ggcagtgcca gccgaagtct gccgttggcc aagaggcccc ggctggcgcg
781 tgcccctgag ccggagcgga cgcccgctgg gcaggggtcc tgggcccacc cgggacggac
841 gcgtggacgg agtgacgtgc gttctcgtgg ggtgtcacct gccagaccgc ccgaagaagc
901 cacctctttg gaggggtgctg tctctggcac gcgccactcc caccatccg tgggcccgca
961 gcaccacgct ggccccccat ccacatcgcg gccaccacgt ccctgggaca cgccttgtcc
1021 cccggtgtac gccgagacca agcacttccg ctactcctca ggcgacagg ggcgctcgga
1081 gccctccttc ctactcagct ctctgaggcc cagcctgact ggctcgtgga ggctcgtgga
1141 gaccatcttt ctgggttcca ggccttggat gccagggact ccccgaggt tgccccgcct
1201 gccccagcgc tactggcaaa tgcggccctc gttcttggag ctgcttggga accacgcgca
1261 gtgcccctac ggggtgctcc tcaagacgca ctgcccgtg cgagctggcg taccaccagc
1321 agccggtgtc tgtgcccggg agaaagcccc gggctctgtg gcggcccccg aggaggagga
1381 cacagacccc cgctgcctgg tgcagctgct ccgccagcac agcagccctc ggaggtgta
1441 cggcttcgtg cgggcctgcc tgcgcgggct ggtgccccca ggctctggg gctccaggca
1501 caacgaacgc cgcttccctc ggaacaccaa gaagtccatc tccctgggga agcatgccaa
1561 gctctcgctg caggagctga cgtggaagat gagcgtgctg gactgctgtt ggctgctgag
1621 gagcccaggg gttggctgtg ttccggccgc agagcacctg ctgctgagg agatctggc
1681 caagtctctg cactggctga tgagtgtgta cgctgctgag ctgctcaggt cttctcttta
1741 tgtcacggag accacgtttc aaaagaacag gctctttttc taccggaaga gtgtctggag
1801 caagtgtcaa agcattggaa tcagacagca cttgaagagg gtgagctgct gggagctgtc
1861 ggaagcagag gtcaggcagc atcggaagac caggcccgcg ctgctgacgt ccagactccg
1921 cttcatcccc aagcctgacg gcgtgcggcc gattgtgaac atggactacg tgcgtgggagc
1981 cagaacgttc cgcagagaaa agaggggcca gcgtctcacc tcgagggtga aggcactgtt
2041 cagcgtgctc aactacgagc gggcgccggc ccccgccctc ctgggcgctc ctgtgctggg
2101 cctggacgat atccacaggg cctggcgcac cttcgtgctg cggtgcgggg cccaggacc
2161 gccgcctgag ctgtactttg tcaaggtgga tgtgacgggc gcgtacgaca ccatccccca
2221 ggagaggtc acggaggtca tcgcagcat catcaaacc cagaacacgt actgctgctg
2281 tcggtatgcc gtggtccaga aggcgcgcca tgggcacgtc cgcaaggcct tcaagagcca
2341 cgtctctacc ttgacagacc tccagccgta catgagacag ttcgtggctc acctgcagga
2401 gaccagcccg ctgagggtat ccgtgctcat cgagcagagc tccctccctg atgaggccag
2461 cagtggcctc ttccagctct cctacgctt catgtgccac cagcccgctg gcatcagggg
2521 caagtcttac gtccagtgcc aggggactcc gcagggtccc atcctctcca cgtgctctg
2581 cagcctgtgc tacggcgaca tggagaacaa gctgtttgct gggattcggc gggacgggct
2641 gctcctgctg ttggtgggat atttcttgtt ggtgacacct caccacccc accgaaaaac
2701 cttcctcagg accctggtcc gaggtgtccc tgagtatggc tgcgtgggta acttgcgga
2761 gacagtgggt aacttccctg tagaagacga ggccttgggt ggcacggctt ttgttcagat
2821 gccggcccac ggccattacc cctggtgccc cctgctgctg gatacccgga cctggaggt
2881 gcagagcgac tactccagct atgcccggac ctccatcaga gccagtctca ccttcaaccg
2941 cggcttcaag gctgggagga acatgcgtcg caaactcttt ggggtcttgc ggctgaagt
3001 tcacagcctg tttctggatt tgcaggtgaa cagcctccag acggtgtgca ccaacatcta
3061 caagatcctc ctgctgcagg cgtacaggtt tcacgcaggt gtgctgcagc tcccatttca
3121 tcagcaagtt tggaaagaacc ccacattttt cctgcgcgtc atctctgaca cggcctccct
3181 ctgctactcc atcctgaaag ccaagaacgc agggatgtcg ctgggggcca agggcgccgc
3241 cggccctctg ccctccgagg ccgtgcagtg gctgtgccac caagcattcc tgctcaagct
3301 gactcgacac cgtgtcacct acgtgccact cctgggggtc ctcaggacag cccagacgca
3361 gctgagtcgg aagctcccgg ggacgaagct gactgccctg gaggcgcgag ccaaccggc
3421 actgccctca gacttcaaga ccatcctgga ctgatggcca cccgcccaca gccaggccga
3481 gagcagacac cagcagccct gtcacgcggg gctctacgtc ccagggaggg agggggcgcc
3541 cacaccagg cccgcaccgc tgggagctcg aggcctgagt gaggtgtcca cggagcctg
3601 catgtccggc tgaaggctga gtgtccggct gaggcctgag cgagtgtcca gccaagggct
3661 gagtgtccag cacacctgcc gtcttcaact cccacagggc tggcgctcgg ctccaccca
3721 gggccagctt ttcctcacca ggagcccggc tccactccc cacataggaa tagtccatcc
3781 ccagattcgc cattgttcac cctgcgccct gccctccttt gccttccacc cccaccatcc
3841 aggtggagac cctgagaagg accctgggag ctctgggaat ttggagtgac caaaggtgtg
3901 ccctgtacac aggcgaggac cctgcacctg gatgggggtc cctgtgggtc aaattggggg
3961 gaggtgctgt gggagtaaaa tactgaatat atgagttttt cagttttgaa aaaaa

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FIG. 16

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MPRAPRCRAVRSLLRSHYREVLPLATFVRRRLGPQGWRLVQRGDP
 AAFRALVAQCLVCVPWDARPPPAAPSFRQVSCLKELVARVLQRL
 CERGAKNVLAFGFALLDGARGGPPEAFTTSVRSYLPNTVTDALR
 GSGAWGLLLRRVGDDVLVHLLARCALFVLVAPSCAYQVCGPPLY
 QLGAATQARPPPHASGPRRRLGCERAWNHSVREAGVPLGLPAPG
 ARRRGGSASRSLPLPKRPRRGAAPEPERTPVGQGSWAHPGRTRG
 PSDRGFCVVSPARPAEEATSLEGALSGTRHSHPSVGRQHHAGPP
 STSRPPRPWDTPCPPVYAETKHFYSSGDKEQLRPSFLLSSLRP
 SLTGARRLVETIFLGSRPWMPGTPRRLPRLPQRYWQMRPLFLEL
 LGNHAQCPYGVLLKTHCPLRAAVTPAAGVCAREKPQGSVAAPPEE
 EDTDPRRLVQLLRQHSSPWQVYGFVRACLRRLVPPGLWGSRHNE
 RRFLRNTKKFISLGKHAKLSLQELTWKMSVRDCAWLRRSPGVGC
 VPAAEHRLREEILAKFLHWMMSVYVVELLRSFFYVTETTFQKNR
 LFFYRKSVMKLSQSIGIRQHLKRVQLRELSEAEVRQHREARPAL
 LTSRLRFIPKPDGLRPIVNMDYVVGARTFRREKRAERLTSRVKA
 LFSVLNYERARRPGLLGASVLGLDDIHRWRTFVLRVRAQDPPP
 ELYFVKVDVTGAYDTIPQDRLTEVIASIIKPQNTYCVRRYAVVQ
 KAAHGHVRKAFKSHVSTLTDLPYMRQFVAHLQETSPLRDAVVI
 EQSSSLNEASSGLFDVFLRFMCHHAVRIRGKSYVQCQGI PQGSI
 LSTLLCSLCYGD MENKLFAGIRRDGLLLRLVDDFLLVTPHLTHA
 KTFRLTLVRGVPEYGCVVNLKRTVVNFPVEDEALGGTAFVQMPA
 HGLFPWCGLLLDTRTLEVQSDYSSYARTSIRASLTFNRGFKAGR
 NMRRKLFGLVRLKCHSLFLDLQVNSLQTVCTNIYKILLQAYRF
 HACVLQLPFFHQVWKNPTFFLRVISDTASLCYSILKAKNAGMSL
 GAKGAAGPLPSEAVQWLCHQAFLLKLTRHRVTYVPLLGLSLRTAQ
 TQLSRKLPGTTLTALEAAANPALPSDFKTILD

FIG. 17

GGCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTCTTTCTT
 TTATGTACACGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACCGGAAGAGTGTCTG
 GAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAGAGGGTGACGTGCGGGAGCT
 GTCGGAAGCAGAGGTACGGCAGCATCGGGAAGCCAGGCCCCGCCCTGCTGACGTCCAGACT
 CCGCTTCATCCCCAAGCCTGACGGGCTGCGGCCGATTGTGAACATGGACTACGTCTGCGG
 AGCCAGAACGTTCCCGCAGAGAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACT
 GTTCAGCGTGCTCAACTACGAGCGGGCGCGGCCCGCCCTCTGGGCGCCTCTGTGCT
 GGGCCTGGACGATATCCACAGGGCCTGGCGCACCTTCGTGCTGCGTGTCGGGGCCAGGA
 CCCGCCGCTGAGCTGTACTTTGTCAAGGTGGATGTGACGGGCGCGTACGACACCATCCC
 CCAGGACAGGCTCACGGAGGTTCATCGCCAGCATCATCAAACCCAGAACACGTACTGCGT
 CCGTTCGCTATGCCGTGGTCCAGAAGGCCGCCCATGGGCACGTCCGCAAGGCCCTCAAGAG
 CCACGTCCCTACGTCCAGTGCCAGGGGATCCCGCAGGGCTCCATCCTCTCCACGCTGCTCT
 GCAGCCTGTGCTACGGCGACATGGAGAACAAGCTGTTTTCGGGGGATTTCGGCGGGACGGGC
 TGCTCCTGCGTTTGGTGGATGATTTCTTGTGGTGACACCTCACCTCACCCACGCGAAAA
 CCTTCCTCAGGACCTGGTCCGAGGTGTCCCTGAGTATGGCTGCGTGCTGAGTGAACCTGCGGA
 AGACAGTGGTGAACCTTCCCTGTAGAAGACGAGGCCCTGGGTGGCACGGCTTTTGTTCAGA
 TGCCGGCCCCACGGCCTATTCCCTGGTGGCGCCTGCTGCTGGATACCCGGACCTGGAGG
 TGCAGAGCGACTACTCCAGCTATGCCCGGACCTCCATCAGAGCCAGTCTCACCTTCAACC
 GCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAAACTCTTTGGGGTCTTGCGGCTGAAGT
 GTCACAGCCTGTTTCTGGATTGTCAGGTGAACAGCCTCCAGACGGTGTGCACCAACATCT
 ACAAGATCCTCCTGCTGCAGGCGTACAGGTTTTCACGCATGTGTGCTGCAGCTCCCATTTT
 ATCAGCAAGTTTGAAGAACCCACATTTTCTGCGCGTCATCTCTGACACGGCCTCCC
 TCTGCTACTCCATCCTGAAAGCCAAGAAGCAGGGATGTCGCTGGGGGCCAAGGGCGCCG
 CCGGCC7TCTGCCCTCCGAGGCCGTGCAGTGGCTGTGCCACCAAGCATTCCTGCTCAAGC
 TGACTCGACACCGTGTACCTACGTGCCACTCCTGGGGTCACTCAGGACAGCCAGACGC
 AGCTGAGTCGGAAGCTCCCGGGGACGACGCTGACTGCCCTGGAGGCCGACGCCAACCCGG
 CACTGCCCTCAGACTTCAAGACCATCCTGGACTGATGGCCACCCGCCACAGCCAGGCCG
 AGAGCAGACACACAGCAGCCCTGTACGCCCGGGCTCTACGTCCCAGGGAGGGAGGGGCGGC
 CCACACCCAGGCTGCACCGCTGGGAGTCTGAGGCCTGAGTGAGTGTGTTGGCCGAGGCCT
 GCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGCCTGAGCGAGTGTCCAGCCAAAGGC
 TGAGTGTCCAGCACACCTGCCGTCTTCACTTCCCCACAGGCTGGCGCTCGGCTCCACCCC
 AGGGCCAGCTTTTCTCACCAGGAGCCCGGCTTCCACTCCCCACATAGGAATAGTCCATC
 CCCAGATTGCGCATTTGTTACCCCTCGCCCTGCCCTCCTTTGCCTTCCACCCCCACCATC
 CAGGTGGAGACCCTGAGAAGGACCCCTGGGAGCTCTGGGAATTTGGAGTGACCAAAGGTGT
 GCCCTGTACACAGGCGAGGACCCCTGCACCTGGATGGGGGTCCCTGTGGGTCAAATTGGGG
 GGAGGTGCTGTGGGAGTAAAAATACTGAATATATGAGTTTTTTCAGTTTTTG0AAAAAAAAA
 AAAAAAAAAAAAAAAAAA

FIG. 18

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MetSerValTyrValValGluLeuLeuArgSerPhePhe
 TyrValThrGluThrThrPheGlnLysAsnArgLeuPhe
 PheTyrArgLysSerValTrpSerLysLeuGlnSerIle
 GlyIleArgGlnHisLeuLysArgValGlnLeuArgGlu
 LeuSerGluAlaGluValArgGlnHisArgGluAlaArg
 ProAlaLeuLeuThrSerArgLeuArgPheIleProLys
 ProAspGlyLeuArgProIleValAsnMetAspTyrVal
 ValGlyAlaArgThrPheArgArgGluLysArgAlaGlu
 ArgLeuThrSerArgValLysAlaLeuPheSerValLeu
 AsnTyrGluArgAlaArgArgProGlyLeuLeuGlyAla
 SerValLeuGlyLeuAspAspIleHisArgAlaTrpArg
 ThrPheValLeuArgValArgAlaGlnAspProProPro
 GluLeuTyrPheValLysValAspValThrGlyAlaTyr
 AspThrIleProGlnAspArgLeuThrGluValIleAla
 SerIleIleLysProGlnAsnThrTyrCysValArgArg
 TyrAlaValValGlnLysAlaAlaHisGlyHisValArg
 LysAlaPheLysSerHisValLeuArgProValProGly
 AspProAlaGlyLeuHisProLeuHisAlaAlaLeuGln
 ProValLeuArgArgHisGlyGluGlnAlaValCysGly
 AspSerAlaGlyArgAlaAlaProAlaPheGlyGly

FIG. 19

1
met

GCAGCGCTGCGTCCTGCTGCGCACGTGGGAAGCCCTGGCCCCGGCCACCCCCGCG ATG

10

pro arg ala pro arg cys arg ala val arg ser leu leu arg ser
 CCG CGC GCT CCC CGC TGC CGA GCC GTG CGC TCC CTG CTG CGC AGC

20

his tyr arg glu val leu pro leu ala thr phe val arg arg leu
 CAC TAC CGC GAG GTG CTG CCG CTG GCC ACG TTC GTG CGG CGC CTG

30

40

gly pro gln gly trp arg leu val gln arg gly asp pro ala ala
 GGG CCC CAG GGC TGG CGG CTG GTG CAG CGC GGG GAC CCG GCG GCT

50

phe arg ala leu val ala gln cys leu val cys val pro trp asp
 TTC CGC GCG CTG GTG GCC CAG TGC CTG GTG TGC GTG CCC TGG GAC

60

70

ala arg pro pro pro ala ala pro ser phe arg gln val ser cys
 GCA CGG CCG CCC CCC GCC GCC CCC TCC TTC CGC CAG GTG TCC TGC

80

leu lys glu leu val ala arg val leu gln arg leu cys glu arg
 CTG AAG GAG CTG GTG GCC CGA GTG CTG CAG AGG CTG TGC GAG CGC

90

100

gly ala lys asn val leu ala phe gly phe ala leu leu asp gly
 GGC GCG AAG AAC GTG CTG GCC TTC GGC TTC GCG CTG CTG GAC GGG

110

ala arg gly gly pro pro glu ala phe thr thr ser val arg ser
 GCC CGC GGG GGC CCC CCC GAG GCC TTC ACC ACC AGC GTG CGC AGC

120

FIG. 20A

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                                130
tyr leu pro asn thr val thr asp ala leu arg gly ser gly ala
TAC CTG CCC AAC ACG GTG ACC GAC GCA CTG CGG GGG AGC GGG GCG

                                140
trp gly leu leu leu arg arg val gly asp asp val leu val his
TGG GGG CTG CTG CTG CGC CGC GTG GGC GAC GAC GTG CTG GTT CAC

                                150

leu leu ala arg cys ala leu phe val leu val ala pro ser cys
CTG CTG GCA CGC TGC GCG CTC TTT GTG CTG GTG GCT CCC AGC TGC

                                160

ala tyr gln val cys gly pro pro leu tyr gln leu gly ala ala
GCC TAC CAG GTG TGC GGG CCG CCG CTG TAC CAG CTC GGC GCT GCC

                                170
                                180
thr gln ala arg pro pro pro his ala ser gly pro arg arg arg
ACT CAG GCC CGG CCC CCG CCA CAC GCT AGT GGA CCC CGA AGG CGT

                                190

leu gly cys glu arg ala trp asn his ser val arg glu ala gly
CTG GGA TGC GAA CGG GCC TGG AAC CAT AGC GTC AGG GAG GCC GGG

                                200
                                210
val pro leu gly leu pro ala pro gly ala arg arg arg gly gly
GTC CCC CTG GGC CTG CCA GCC CCG GGT GCG AGG AGG CGC GGG GGC

                                220

ser ala ser arg ser leu pro leu pro lys arg pro arg arg gly
AGT GCC AGC CGA AGT CTG CCG TTG CCC AAG AGG CCC AGG CGT GGC

                                230
                                240
ala ala pro glu pro glu arg thr pro val gly gln gly ser trp
GCT GCC CCT GAG CCG GAG CGG ACG CCC GTT GGG CAG GGG TCC TGG

                                250

ala his pro gly arg thr arg gly pro ser asp arg gly phe cys
GCC CAC CCG GGC AGG ACG CGT GGA CCG AGT GAC CGT GGT TTC TGT

                                260
                                270
val val ser pro ala arg pro ala glu glu ala thr ser leu glu
GTG GTG TCA CCT GCC AGA CCC GCC GAA GAA GCC ACC TCT TTG GAG

                                280

gly ala leu ser gly thr arg his ser his pro ser val gly arg
GGT GCG CTC TCT GGC ACG CGC CAC TCC CAC CCA TCC GTG GGC CGC

                                290
                                300
gln his his ala gly pro pro ser thr ser arg pro pro arg pro
CAG CAC CAC GCG GGC CCC CCA TCC ACA TCG CGG CCA CCA CGT CCC

                                310

trp asp thr pro cys pro pro val tyr ala glu thr lys his phe
TGG GAC ACG CCT TGT CCC CCG GTG TAC GCC GAG ACC AAG CAC TTC

                                320
                                330

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FIG. 20B

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                                340
leu tyr ser ser gly asp lys glu gln leu arg pro ser phe leu
CTC TAC TCC TCA GGC GAC AAG GAG CAG CTG CGG CCC TCC TTC CTA

                                350
leu ser ser leu arg pro ser leu thr gly ala arg arg leu val
CTC AGC TCT CTG AGG CCC AGC CTG ACT GGC GCT CGG AGG CTC GTG

                                360
                                370
glu thr ile phe leu gly ser arg pro trp met pro gly thr pro
GAG ACC ATC TTT CTG GGT TCC AGG CCC TGG ATG CCA GGG ACT CCC

                                380
                                390
arg arg leu pro arg leu pro gln arg tyr trp gln met arg pro
CGC AGG TTG CCC CGC CTG CCC CAG CGC TAC TGG CAA ATG CGG CCC

                                400
leu phe leu glu leu leu gly asn his ala gln cys pro tyr gly
CTG TTT CTG GAG CTG CTT GGG AAC CAC GCG CAG TGC CCC TAC GGG

                                410
                                420
val leu leu lys thr his cys pro leu arg ala ala val thr pro
GTG CTC CTC AAG ACG CAC TGC CCG CTG CGA GCT GCG GTC ACC CCA

                                430
ala ala gly val cys ala arg glu lys pro gln gly ser val ala
GCA GCC GGT GTC TGT GCC CGG GAG AAG CCC CAG GGC TCT GTG GCG

                                440
                                450
ala pro glu glu glu asp thr asp pro arg arg leu val gln leu
GCC CCC GAG GAG GAG GAC ACA GAC CCC CGT CGC CTG GTG CAG CTG

                                460
leu arg gln his ser ser pro trp gln val tyr gly phe val arg
CTC CGC CAG CAC AGC AGC CCC TGG CAG GTG TAC GGC TTC GTG CGG

                                470
                                480
ala cys leu arg arg leu val pro pro gly leu trp gly ser arg
GCC TGC CTG CGC CGG CTG GTG CCC CCA GGC CTC TGG GGC TCC AGG

                                490
his asn glu arg arg phe leu arg asn thr lys lys phe ile ser
CAC AAC GAA CGC CGC TTC CTC AGG AAC ACC AAG AAG TTC ATC TCC

                                500
                                510
leu gly lys his ala lys leu ser leu gln glu leu thr trp lys
CTG GGG AAG CAT GCC AAG CTC TCG CTG CAG GAG CTG ACG TGG AAG

                                520
met ser val arg asp cys ala trp leu arg arg ser pro gly val
ATG AGC GTG CGG GAC TGC GCT TGG CTG CGC AGG AGC CCA GGG GTT

                                530
                                540
gly cys val pro ala ala glu his arg leu arg glu glu ile leu
GGC TGT GTT CCG GCC GCA GAG CAC CGT CTG CGT GAG GAG ATC CTG

```

FIG. 20C

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                    550
ala lys phe leu his trp leu met ser val tyr val val glu leu
GCC AAG TTC CTG CAC TGG CTG ATG AGT GTG TAC GTC GTC GAG CTG

                    560
leu arg ser phe phe tyr val thr glu thr thr phe gln lys asn
CTC AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC

                    570
                    580
arg leu phe phe tyr arg lys ser val trp ser lys leu gln ser
AGG CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC

                    590
ile gly ile arg gln his leu lys arg val gln leu arg glu leu
ATT GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG

                    600
                    610
ser glu ala glu val arg gln his arg glu ala arg pro ala leu
TCG GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG

                    620
leu thr ser arg leu arg phe ile pro lys pro asp gly leu arg
CTG ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG

                    630
                    640
pro ile val asn met asp tyr val val gly ala arg thr phe arg
CCG ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC

                    650
arg glu lys arg ala glu arg leu thr ser arg val lys ala leu
AGA GAA AAG AGG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG

                    660
                    670
phe ser val leu asn tyr glu arg ala arg arg pro gly leu leu
TTC AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG

                    680
gly ala ser val leu gly leu asp asp ile his arg ala trp arg
GGC GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC

                    690
                    700
thr phe val leu arg val arg ala gln asp pro pro pro glu leu
ACC TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG

                    710
tyr phe val lys val asp val thr gly ala tyr asp thr ile pro
TAC TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC

                    720
                    730
gln asp arg leu thr glu val ile ala ser ile ile lys pro gln
CAG GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG

                    740
asn thr tyr cys val arg arg tyr ala val val gln lys ala ala
AAC ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC

                    750

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FIG. 20D

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his gly his val arg lys ala phe lys ser his val leu arg pro
CAT GGG CAC GTC CGC AAG GCC TTC AAG AGC CAC GTC CTA CGT CCA

760

val pro gly asp pro ala gly leu his pro leu his ala ala leu
GTG CCA GGG GAT CCC GCA GGG CTC CAT CCT CTC CAC GCT GCT CTG

770

gln pro val leu arg arg his gly glu gln ala val cys gly asp
CAG CCT GTG CTA CGG CGA CAT GGA GAA CAA GCT GTT TGC GGG GAT

790

ser ala gly arg ala ala pro ala phe gly gly OP
TCG GCG GGA CGG GCT GCT CCT GCG TTT GGT GGA TGA TTTCTTGTTGGT

800

807

GACACCTCACCTCACCCACGCGAAAACCTTCCTCAGGACCCTGGTCCGAGGTGTCCCTGA
GTATGGCTGCGTGTTGAAGTTCGCGAAGACAGTGGTGAAGTTCCTGTAGAAGACGAGGC
CCTGGGTGGCACGGCTTTTGTTCAGATGCCGCCCCACGGCCTATTCCCCTGGTGCGGCCT
GCTGCTGGATACCCGGACCCTGGAGGTGCAGAGCGACTACTCCAGCTATGCCCGGACCTC
CATCAGAGCCAGTCTCACCTTCAACCGCGGCTTCAAGGCTGGGAGGAACATGCGTCGCAA
ACTCTTTGGGGTCTTGCGGCTGAAGTGTACAGCCTGTTTCTGGATTTGCAGGTGAACAG
CCTCCAGACGGTGTGCACCAACATCTACAAGATCCTCCTGCTGCAGGCGTACAGGTTTCA
CGCATGTGTGCTGCAGCTCCCATTTTCATCAGCAAGTTTGGAAGAACCCACATTTTTCCT
GCGCGTCATCTCTGACACGGCCTCCCTCTGCTACTCCATCCTGAAAGCCAAGAACGCAGG
GATGTGCTGCTGGGGGCCAAGGGCGCCGCGGCCCTCTGCCCTCCGAGGCGGTGCAGTGGCT
GTGCCACCAAGCATTCTGCTCAAGCTGACTCGACACCGTGTACCTACGTGCCACTCCT
GGGGTCACTCAGGACAGCCCAGACGCAGCTGAGTCGGAAGCTCCCGGGGACGACGCTGAC
TGCCCTGGAGGCCGACAGCCAACCCGGCACTGCCCTCAGACTTCAAGACCATCCTGGACTG
ATGGCCACCCGCCCACAGCCAGGCCGAGAGCAGACACCAGCAGCCCTGTACGCCGGGCT
CTACGTCCCAGGGAGGGAGGGGCGGCCACACCCAGGCCCGCACCGCTGGGAGTCTGAGG
CCTGAGTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAG
GCCTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCCGTCTTCACTTCCC
CACAGGCTGGCGCTCGGCTCCACCCAGGGCCAGCTTTTCTCTACCAGGAGCCCGGCTTC
CACTCCCCACATAGGAATAGTCCATCCCCAGATTGCGCATTTGTTACCCCTCGCCCTGCC
CTCCTTTGCCTTCCACCCCAACCATCCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTC
TGGGAATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGAT
GGGGGTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATG
AGTTTTTTCAGTTTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIG. 20E

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FIG. 21A

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4321 GGTGTTTTTAAGCCAATNANAAAATTTTTTNATGTTGTTNNNNNNNNNNNNNNNNNNNN
CCACAAAATTCGGTTANTNTTTTAAAAAANTACAACAAANNNNNNNNNNNNNNNNNNNN

4381 NNN
NN

4441 NNN
NN

4501 NNN
NN

4561 NNN
NN

4621 NNN
NN

4681 NNN
NN

4741 NNN
NN

4801 NNN
NN

4861 NNN
NN

4921 NNN
NN

4981 NNN
NN

5041 NGCCANGRAGGGGGCCAGGTTCCAANTTCCAACCKTTTWWGGARGGACNGCCCCAGGG
NCGGTNCYTCCCCCGGTCCAAGGTTNAAGGGTTGGMAAAAWCCTYCCTGNCGGGGGTCCC

5101 GGGGATRAACAGANTNGGGGGKGGTWGGGTTNAKGGTGGGAACNCCTTNGCGCCTGGAG
CCCCTAYTTGTCTNANCCCCCMCCAWCCCAANTMCCACCCCTGNGGAANCGSCGGACCTC

5161 AACGTGCAAAGAGGAAATGAAGGGCCTGKGTCAAGGAGCCCAAGTNGGCGGGGRAGTTTG
TTGCACGTTTCTCCTTTACTTCCCGGACMCAGTTCCTCGGGTTCANCCGCCCCYTCAAAC

5221 CAGGGAGGCACTCCGGGGAGGTCCSGCGTGCCCGTCCAAGGGAGCAATGCGTCCTTCGGG
GTCCCTCCGTGAGGCCCTCCAGGSCGCACGGGCAGGTTCCCTCGTTACGCAGGAAGCCC

5281 TTCGTCCCCAWGCCGCGTCTACGCGCCTYCCGTCCCTCCCCTTCACGTTCCGGCATTCGTG
AAGCAGGGGTWCGGCGCAGATGCGCGGARGGCAGGAGGGGAAGTGCAAGGCCGTAAGCAC

5341 GTGCCCCGAGCCCGACGCCCGCGTCCGGACCTGGAGGCAGCCCTGGGTCTCCGGATCAG
CACGGGCCTCGGGCTGCGGGGCGCAGGCCCTGGACCTCCGTGCGGACCCAGAGGCCTAGTC

5401 GCCAGCGGCCAAAGGGTCGCCGCACGCACCTGTTCCAGGGCCTCCACATCATGGCCCCCT
CGGTCGCCGGTTTCCAGCGGCGTGCGTGGACAAGGGTCCCGGAGGTGTAGTACCGGGGA

FIG. 21B

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5461 CCCTCGGGTTACCCACAGCCTAGGCCGGATTTCGACCTCTCTCCGCTGGGGCCCTCGCCT
GGGAGCCCAATGGGGTGTCTGGATCCGGCCTAAGCTGGAGAGAGGCGACCCCGGGAGCGGA

Sp1

5521 GGCCTCCCTGCACCCTGGGAGCGCGAGCGGCGCGGGCGGGGAAGCGCGGCCCATACCC
CCGCAGGGACGTGGGACCCTCGCGCTCGCCGCGCGCCCGCCCCTTCGCGCCGGGTATGGG

5581 CCGGGTCCGCCCCGAAGCAGCTGCGCTGTCTGGGGCCAGGCCGGGCTCCCAGTGGATTTCG
GGCCAGGCGGGCCTTCGTCTGACGCGACAGCCCCGGTCCGGCCCCGAGGGTCACCTAAGCG

Topo_II_cleavage_site

5641 GGGCACAGACGCCCAGGACCGCGCTTCCACGTGGCGGAAGGACTGGGGACCCGGGCACC
CCCCTGTCTGCGGGTCTGGCGCGAAGGGTGACCGCCTTCTGACCCCTGGGCCCCGTGG

E2F

5701 CGTCCTGCCCCCTTACCTTCCAGCTCCGCTTCTTCCGCGCGGACCCGGCCCCGTCCCGAA
GCAGGACGGGGAAGTGGAAGGTGAGGCGAAGAAGGCGCGCCTGGGCGGGGCGAGGGCTT

E

5761 CCCTTCCCAGGTCCCGGCCCAGCCCCCTTCCGGGCCCTCCCAGCCCCCTCCCCTTCTTTTC
GGGAAGGGTCCAGGGCCGGGTCTGGGGAAGCCCCGGGAGGGTCTGGGAGGGGAAGGAAAAG

Sp1

=====

2F

NFkB

h

5821 CGCGGCCCCCGCCCTCTCCTTCGCGGCGCGAGTTTCAGGCAGCGCTGCGTCCTGCTGCGCA
CGCCCGGGGCGGGAGAGGAAGCGCCGCGCTCAAAGTCCGTCGCGACGCAGGACGACGCGT

5860

ECO47III

5875

FSP1

TRT5'

*****>

5881 CGTGGGAAGCCCTGGCCCCGGCCACCCCGCGATGCCGCGCGCTCCCCGCTGCCGAGCCG
GCACCCCTTCGGGACCGGGGCCGGTGGGGGCGCTACGGCGCGCGAGGGGCGACGGCTCGGC

5941 TGCCTCCCTGCTGCGCAGCCACTACCGCGAGGTGCTGCCGCTGGCCACGTTTCGTGCGGC
ACGCGAGGGACGACGCGTCTGGTGATGGCGCTCCACGACGGCGACCGGTGCAAGCACGCCG

5953

FSP1

6001 GCCTGGGGCCCCAGGGCTGGCGGCTGGTGACGCGGGGACCCGGCGGCTTTCCGCGCGC
CGGACCCCGGGGTCCCGACCGCCGACACGTCTCGCCCCCTGGGCCGCCGAAAGGCGCGCG

6061 TGGTGGCCAGTGCTGGTGTGCGTGCCCTGGGACGCACGGCCGCCCCCGCGCCCCCT
ACCACCGGGTCACGGACCACACGCACGGGACCCTGCGTGCCGGCGGGGGCGGCGGGGA

NFkB

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FIG. 21C

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*****
6121 CCTTCCGCCAGGTGGGCCTCCCGGGGTCGGCGTCCGGCTGGGGTTGAGGGCGGCCGGGG
    GGAAGGCGGTCCACCCGGAGGGGCCCCAGCCGCAGGCCGACCCCAACTCCCGCCGGCCCC

                                         Topo_II_cleavage_s
                                         ::::::::::::::::::::
                                         NFkB
                                         =====

Intron1
*****>
6181 GGAACCAGCGACATGCGGAGAGCAGCGCAGGCGACTCAGGGCGCTTCCCCCGCAGGTGTC
    CCTTGGTCGCTGTACGCCTCTCGTCGCGTCCGCTGAGTCCCGCGAAGGGGGCGTCCACAG

ite
:

6241 CTGCCTGAAGGAGCTGGTGGCCCGAGTGCTGCAGAGGCTGTGCGAGCGCGGCGCGAAGAA
    GACGGACTTCCTCGACCACCGGGCTCACGACGTCTCCGACACGCTCGCGCCGCGCTTCTT

6301 CGTGCTGGCCTTCGGCTTCGCGCTGCTGGACGGGGCCCGCGGGGGCCCCCGAGGCCCTT
    GCACGACCGGAAGCCGAAGCGCGACGACCTGCCCGGGCGCCCCCGGGGGGCTCCGGA

6361 CACCACCAGCGTGCGCAGCTACCTGCCCAACACGGTGACCGACGCACTGCGGGGGAGCGG
    GTGGTGGTCGCACGCGTCGATGGACGGGTGTGCCACTGGCTGCGTGACGCCCCCTCGCC
    ^
    6372
    FSP1

6421 GGCCTGGGGGCTGCTGCTGCGCCGCGTGGGCGACGACGTGCTGGTTACCTGCTGGCAGC
    CCGCACCCCCGACGACGACGCGGCGCACCCGCTGCTGCACGACCAAGTGGACGACCGTGC

6481 CTGCGCGCTCTTTGTGCTGGTGGCTCCCAGCTGCGCCTACCAGGTGTGCGGGCCGCGCT
    GACGCGCGAGAAACAGACCACCGAGGGTCGACGCGGATGGTCCACACGCCCGGCGGCGA

6541 GTACCAGCTCGGCGCTGCCACTCAGGCCCGGCCCCCGCCACACGCTAGTGGACCCCGAAG
    CATGGTCGAGCCGCGACGGTGAGTCCGGGCCGGGGCGGTGTGCGATCACCTGGGGCTTC

6601 GCGTCTGGGATGCGAACGGGCCTGGAACCATAGCGTCAGGGAGGCCGGGTCCCCCTGGG
    CGCAGACCCTACGCTTGCCCGGACCTTGGTATCGCAGTCCCTCCGGCCCCAGGGGGACCC

6661 CCTGCCAGCCCCGGGTGCGAGGAGGCGCGGGGCGAGTGCCAGCCGAAGTCTGCCGTGTC
    GGACGGTCGGGGCCCACGCTCCTCCGCGCCCCCGTCACGGTCGGCTTCAGACGGCAACGG

6721 CAAGAGGCCCAGGCGTGGCGCTGCCCCCTGAGCCGGAGCGGACGCCCCGTTGGGCAGGGGTC
    GTTCTCCGGGTCCGCACCGCGACGGGGACTCGGCCTCGCCTGCGGGCAACCCGTCCCCAG

6781 CTGGGCCCCACCCGGGCAGGACGCGTGACCGAGTGACCGTGTTTCTGTGTGGTGTACCC
    GACCCGGGTGGGCCCCGTCCTGCGCACCTGGCTCACTGGCACCAAAGACACACCACAGTGG

6841 TGCCAGACCCGCCGAAGAAGCCACCTCTTTGGAGGGTGCGCTCTCTGGCACGCGCCACTC
    ACGGTCTGGGCGGCTTCTTCGGTGGAGAAACCTCCACGCGAGAGACCGTGCGCGGTGAG

6901 CCACCCATCCGTGGGCCGCCAGCACACGCGGGCCCCCATCCACATCGCGGCCACCACG
    GGTGGGTAGGCACCCGCGGTCGTGGTGCGCCGGGGGGTAGGTGTAGCGCCGGTGGTGC

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FIG. 21D

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6961 TCCCTGGGACACGCCTTGTCCCCCGGTGTACGCCGAGACCAAGCACTTCCTCTACTCCTC
AGGGACCCTGTGCGGAACAGGGGGCCACATGCGGCTCTGGTTCGTGAAGGAGATGAGGAG

7021 AGGCGACAAGGAGCAGCTGCGGCCCTCCTTCCTACTCAGCTCTCTGAGGCCCAGCCTGAC
TCCGCTGTTTCTCGTCGACGCCGGGAGGAAGGATGAGTCGAGAGACTCCGGGTGCGACTG

7081 TGGCGCTCGGAGGCTCGTGGAGACCATCTTTCTGGGTTCAGGCCCTGGATGCCAGGGAC
ACCGCGAGCCTCCGAGCACCTCTGGTAGAAAGACCCAAGGTCCGGGACCTACGGTCCCTG

7141 TCCCCGCAGGTTGCCCCGCCTGCCCCAGCGCTACTGGCAAATGCGGCCCTGTTTCTGGA
AGGGGCGTCCAACGGGGCGGACGGGGTCGCGATGACCGTTTACGCCGGGGACAAAGACCT
^
7167
ECO47III

7201 GCTGCTTGGGAACCACGCGCAGTGCCCCCTACGGGGTGCTCCTCAAGACGCACTGCCCCGT
CGACGAACCCTTGGTGCGCGTCACGGGGATGCCCCACGAGGAGTTCTGCGTGACGGGCGA

7261 GCGAGCTGCGGTACCCCCAGCAGCCGGTGTCTGTGCCCGGGAGAAGCCCCAGGGCTCTGT
CGCTCGACGCCAGTGCGGTGCGTCCGCCACAGACACGGGCCCTCTTCGGGGTCCCGAGACA

7321 GCGGGCCCCCGAGGAGGAGACACAGACCCCCGTGCGCTGGTGCAGCTGCTCCGCCAGCA
CCGCCGGGGGCTCCTCCTCTGTGTCTGGGGGCGAGCGGACCACGTCGACGAGGCGGTCTGT

7381 CAGCAGCCCCCTGGCAGGTGTACGGCTTCGTGCGGGCCTGCCTGCGCCGGCTGGTGCCCCC
GTCGTGCGGGGACCGTCCACATGCCGAAGCACGCCCGGACGGACGCGGCCGACACGGGGG

7441 AGGCCTCTGGGGCTCCAGGCACAACGAACGCCGCTTCCTCAGGAACACCAAGAAGTTCAT
TCCGGAGACCCCCGAGTCCGTGTTGCTTGCGGCGAAGGAGTCTTGTTGGTTCTTCAAGTA

7501 CTCCCTGGGGAAGCATGCCAAGCTCTCGCTGCAGGAGCTGACGTGGAAGATGAGCGTGCG
GAGGGACCCCTTCGTACGGTTCGAGAGCGACGTCCTCGACTGCACCTTCTACTCGCACCG

*****
7561 GGACTGCGCTTGGCTGCGCAGGAGCCCAGGTGAGGAGGTGGTGGCCGTGAGGGCCCAGG
CCTGACGCGAACCGACGCGTCTCGGGTCCACTCCTCCACCACCGGCAGCTCCCGGGTCC
^
7575
FSP1

Intron2
*****
7621 CCCCAGAGCTGAATGCAGTAGGGGCTCAGAAAAGGGGGCAGGCAGAGCCCTGGTCCTCCT
GGGTCTCGACTTACGTTCATCCCCGAGTCTTTTCCCCCGTCCGTCTCGGGACCAGGAGGA

*****
7681 GTCTCCATCGTCACGTGGGCACACGTGGCTTTTTCGCTCAGGACGTGAGTGGACACGGTG
CAGAGGTAGCAGTGCACCCGTGTGCACCGAAAAGCGAGTCTTGCAGCTCACCTGTGCCAC

**>
7741 ATCGAGGTGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTCGTAATCATGGTCATA
TAGCTCCAGCTGAGATCTCCTAGGGGCCCATGGCTCGAGCTTAAGCATTAGTACCAGTAT
^
7747
SAL1

```

FIG. 21E

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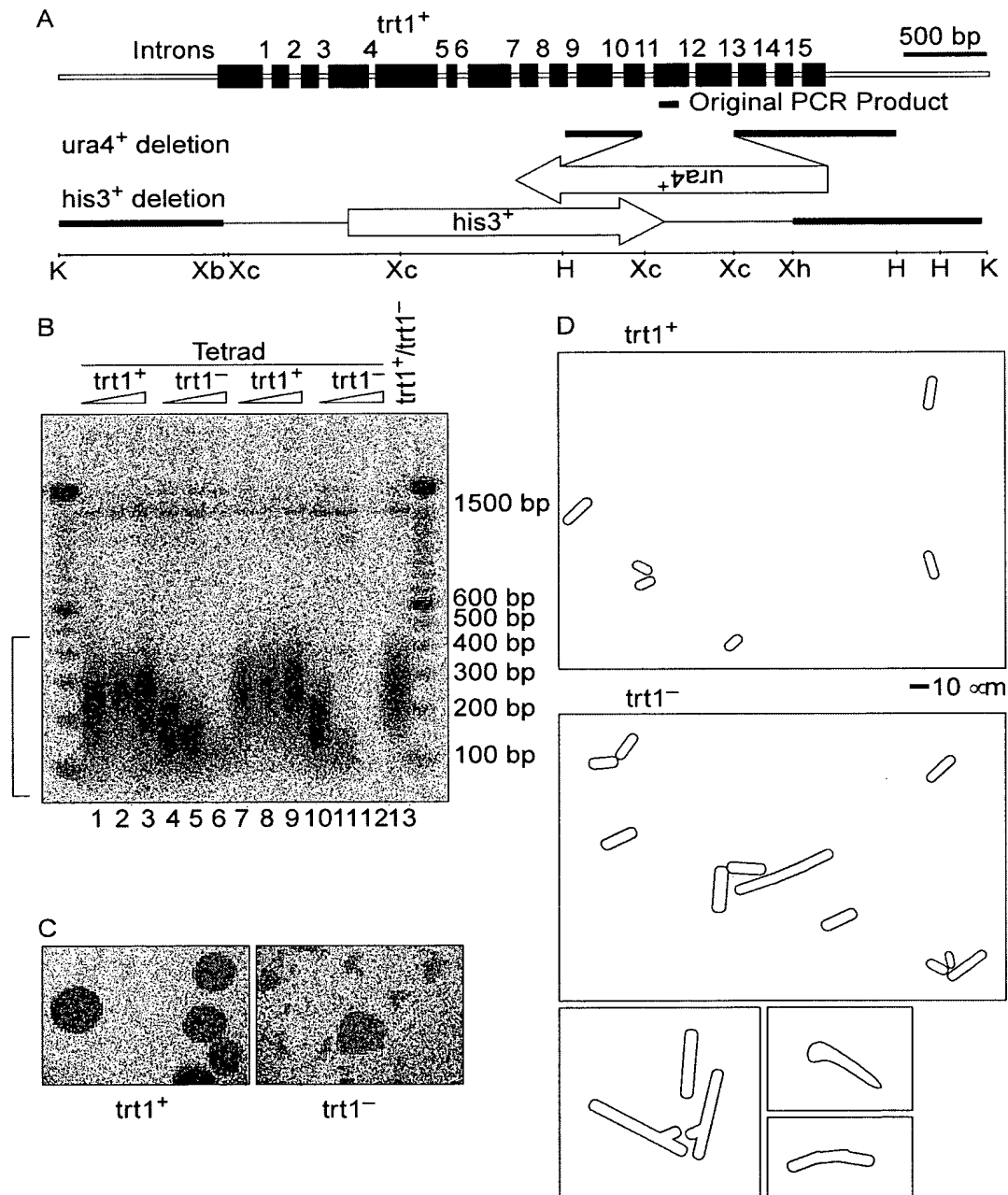


FIG. 22

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gccaaagtctcctgcactggctgatgagtggtacgtcgtcgagctgctcaggtctttcttt
tatgtcacggagaccacgtttcaaaagaacaggctctttttctaccggaagagtgtctgg
agcaagttgcaaagcattggaatcagacagcacttgaagaggggtgcagctgcgggacgtg
tcggaagcagaggtcaggcagcatcgggaagccaggcccgccctgctgacgtccagactc
cgcttcatccccaaagcctgacgggctgcggccgattgtgaacatggactacgtcgtggga
gccagaacgttcgcagagaaaaagagggccgagcgtctcacctcgaggggtgaaggcactg
ttcagcgtgctcaactacgagcgggcg

FIG. 23

TCTACCTTGACAGACCTCCAGCCGTACATGCGACAGTTCGTGGCTCACCTGCAGGAG
ACCAGCCCGCTGAGGGATGCCGTCGTTCATCGAGCAGAGCTCCTCCCTGAATGAGGCC
AGCAGTGGCCTCTTCGACGTCTTCCTACGCTTCATGTGCCACCACGCCGTGCGCATC
AGGGGCAAGTC

FIG. 24

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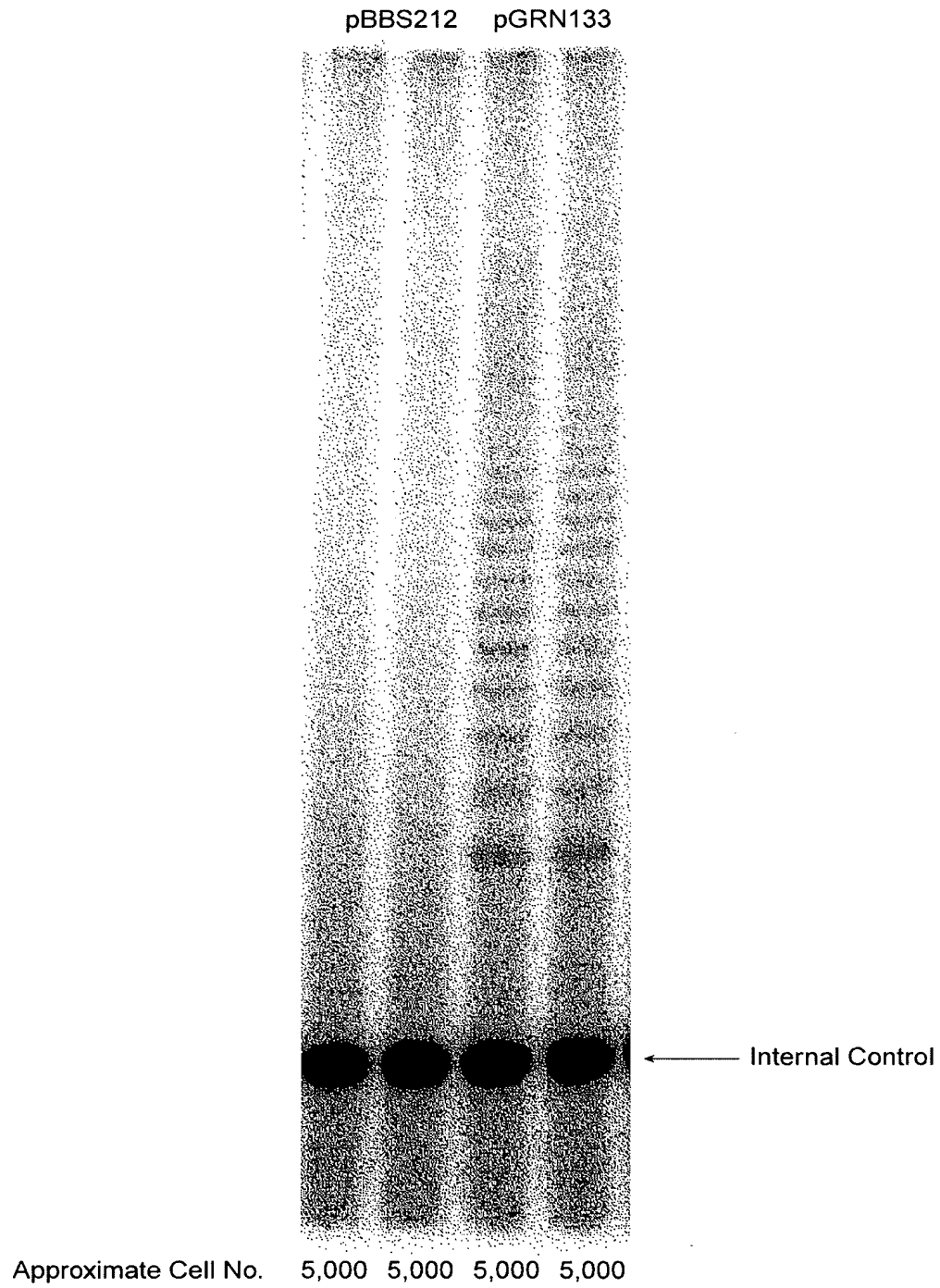


FIG. 25

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